

```

RESULT 1
ab015639
; TOIG of: ab015639 check: 3818 from: 1 to: 2052
;
; LOCUS AB015639 2052 bp mRNA
; DEFINITION Homo sapiens ASY mRNA, complete cds.
; ACCESSION AB015639
; VERSION AB015639.1 GI:5821139
; KEYWORDS ASY.
; SOURCE Homo sapiens (human)
; ORGANISM Homo sapiens
; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
; REFERENCE 1 (bases 1 to 2052)
; AUTHORS Yutsudo,M.

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Qy 153 -----ProGlnAlaGluProValTyrThrProPro---- 162
Db 133 ACGCGGGCTGCGCGCGGGGTGGGCTGTCCGAGGACGAGACGAGGAGACTGGTCCAGGT 74
Qy 163 -----AlaProAlaProAlaAlaProProSerThr 172
Db 73 CTTCCATGGCTGGAGGGTGGAGATGATGTCAGCTGTGCCCGCGCGCGGGGCGCGG 14
Qy 173 Ser 173
Db 13 TCT 11

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Search completed: June 22, 2005, 09:17:30
Job time : 2 secs

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Db 673 GCGCGGCTCCCTCCCTCCCGGCGGCGGCTGAGCCCGGAGGAGCCCGTGTGGANC 732
QY 161 ProProAlaProAlaProAlaProSerThrProAlaAlaProLysArgGly 180
Db 733 CCGCCAGCCCGGCTNCCGCGGCGGCGGCTCCACCCGCGCGCCCAAGCGAGGGC 792
QY 181 SerSerGlyAla-----ValVal 186
Db 793 TCCTCGGCTCAGTGGATGAGACCTTTTGTCTTCTCTCTGCACTGAGCCGTGTGATA 852
QY 187 *****CysIleMetAspLeuLysGluGlnProGlyAsnThrIleSerAlaGly 206
Db 853 CGCTCCTCTCAGAGAAATATGGACTTGAAGGAGCAGCCAGTAACACTATTTCGGCTGGT 912
QY 207 GluGluAspPheProSerValLeuLeuLeuThrAlaAlaSer***ProSerLeuSerPro 226
Db 913 CAAGAGATTTCGCATCTGCTCTGCTTGAACACTGCTGCTCTCTCTCTGCTCCT 972
QY 227 LeuSerAlaAlaSerPheLysGluHisGluTyLeuGlyAsnLeuSerThrValLeuPro 246
Db 973 CTCTCAGCCCTCTTTCAAAGAACATGAATACCTTGGTAATTTGTCAACAGTATTACCC 1032
QY 247 ThrGluGlyThrLeuGlnGlnAsnValSerGluAlaSerLysGluValSerGluLysAla 266
Db 1033 ACTGAAGGAACACTTCAAGAAATGTCAAGTGAAGCTTCTTAAGAGGCTCTCAGAGAAGCA 1092
QY 267 LysThrLeuLeuLeuAspArgAspLeuThrGluPheSerGluLeuLeuTySerGluMet 286
Db 1093 AAAACTCTACTCATAGATAGAGATTTAAACAGAGTTTTCAGAAATAGAAATCTCAGAAATG 1152
QY 287 GlySerSerPheSerValSerProLysAlaGluSerAlaValIleValAlaAsnProArg 306
Db 1153 GGATCATGTTTCAGTGTCTCTCCAAAGCAGAACTGCGGTAAATAGTACCAATCTTAGG 1212
QY 307 GluGluIleIleValLysAsnLysAspGluGluGluLysLeuValSerAsnAsnIleLeu 326
Db 1213 GAAGAAATAATCGTGAAAAATAAAGATGAAGAGAGAAAGTTAGTTAGTAAATCAATCATCCTT 1272
QY 327 His**GlnGlnGluLeuProThrAlaLeuThrLysLeuValLysGluAspGluValVal 346
Db 1273 CATAAATCAACAGAGTTTACCTCAGCTCTTACTTAAATTTGGTTAAAGAGGATGAAGTTGTG 1332
QY 347 SerSerGluLysAlaLysAspSerPheAsnGluLysArgValAlaValGluAlaProMet 366
Db 1333 TCTTCAGAAAAGCAAAAGACAGTTTAAATGAAGAGAGACTTCGAGTGGAGCTCCTATG 1392
QY 367 ArgGluGluTyAlaAspPheLysProPheGluArgValTrpGluValLysAspSerLys 386
Db 1393 AGGAGAGAAATGCGAGACTTCAAAACCAATTTGAGCGAGTATGGGAAGTGAAGTAGTAAG 1452
QY 387 GluAspSerAspMetLeuAlaGlyGlyIleGluSerAsnLeuGluSerLysVal 406
Db 1453 GAAGATAGTATGATGTGTGGCTGCTGGAGGTAAATCGAGAGCAACTTGGAAAGTAAAGTG 1512
QY 407 AspLysLysCysPheAlaAspSerLeuGluGlnThrAsnHisGluLysAspSerGluSer 426
Db 1513 GATAAAAAATGTTTGCAGATAGCTTGCACCAACTAATCACCAGAAAAGTATGAGAGT 1572
QY 427 SerAsnAspAspThrSerPheProSerThrProGluGlyIleLysAspArgSerGlyAla 446
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QY 447 TyrIleThrCysAlaProPheAsnProAlaAlaThrGluSerIleAlaThrAsnIlePhe 466
Db 1633 TATATCATGTGCTGCTCCCTTTAAACCCAGCAGCAACTGAGAGCATTGCAACAACTTTTT 1692
QY 467 ProLeuLeuGluAspProThrSerGluAsn**ThrAspGlu-LysLysIleGluGluTy 486
Db 1693 CCTTTGTTAGGATCCTACTTCAGAAAATAAGNCCGATGAAAAAATAATAGAGAAA 1752
QY 486 sLysAlaGlnIleValThrGluLysAsnThrSerThrLysThrSerAsnProPhe-PheVal 506

Db 1753 GAAGGCCAAATAGTAAACAGAGAAGAAATACTAGCACCAAAACATCAAAACCTTTTACTTG 1812
QY 506 aAlaAlaGlnAspSerGluThrAspTyxValThrThrAspAsnLeuThrLysValThrG 526
Db 1813 TAGCACACAGAGATTCTGAGACAGATATGTCAACACAGATAATTTAAACAAAGGTACTG 1872
QY 526 luGluValValAlaAlaAsnMetProGluGlyLeuThrProAspLeuValGlnGluAlaCysG 546
Db 1873 AGGAAGTCGTGGCAACACATGCCTGAAGGCTGACTCCAGATTTTAGTACAGGAAGCATGTG 1932
QY 546 luSerGluLeuAsnGluValThrGlyThrLysIleAlaTyLeuThrLysMetAspLeuV 566
Db 1933 AAAGTCAATTGAATGAAGTTACTGGTACAAAGATTGCTTTATGAACAACAAAATGGACTGG 1992
QY 566 alGlnThrSerGluValMetGlnGluSerLeuTyxProAlaAlaGlnLeuCysProSerP 586
Db 1993 TTCAAACATCAGAAAGTTATGCAAGAGTCACTCTATCTCGAGCACAGCTTTTGGCCCAT 2052
QY 586 heGluGluSerGluAlaThrProSerProValLeuProAspIleValMetGluAlaProL 606
Db 2053 TTGAAGAGTCAGAAAGCTACTCCTTCACAGTTTTCCTGACATTGTATGGAAGACCAT 2112
QY 606 euAsnSerAlaValProSerAlaGlyAlaSerValIleGlnProSerSerSerProLeuG 626
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QY 626 luAlaSerSerValAsnTyxGluSerIleLysHisGluProGluAsnProProProTyxG 646
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QY 705 luMetAlaLysValGluGlnProValProAspHisSerGluLeuValGluAspSerSerP 725
Db 2413 AAATGCAAAAGTTGAACAGCCAGTGCCTGATCATTTCTGAGCTAGTTGAAGATTCTCCAC 2472
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QY 745 luAspGluThrValMetLeuValLysGluSerLeuThrGluThrSerPheGluSerMetI 765
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Db 2653 TGGAAATCTTTTAAAGCTCAGTTTAGATAAACAAAAAGATACCCCTGTTTACCTGATGAAGTTT 2712
QY 805 erThrLeuSerLysLysGluLysIleProLeuGlnMetGluGluLeuSerThrAlaValT 825
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QY 825 YrSerAsnAspAspLeuPheIleSerLysGluAlaGlnIleArgGluThrGluThrPheS 845
Db 2773 ATTTCAATGATGACTTATTTATTTTCTTAAGGAAGCACAGATAAGAGAAACCTGAAACGTTTT 2832
QY 845 erAspSerSerProIleGluIleIleAspGluPheProThrLeuIleSerSerLysThrA 865
Db 2833 CAGATTCATCTCCAATTGAATTTATAGATGAGTTCCTTACATTGATCAGTTCTTAAAACTG 2892

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QY 865 pSerPheSerLysLeuAlaArgGluTyrThrAspLeuGluValSerHisLysSerGluI 885
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QY 905 erLeuLysAsnIleGlnProLysValGluGluLysIleSerPheSerAspPheSerL 925
Db 3013 CTTTGAAGAACAATACACCCAAAGTTGAAGAAATCAGTTTCTCAGATGACCTTTCTA 3072
QY 925 ysAsnGlySerAlaThrSerLysValLeuLeuLeuProAspValSerAlaLeuGlyH 945
Db 3073 AAAATGGGTCTGTACATCAAAAGGTGCTTATTGCTCCAGATGCTTTCTGCTTTGGCC- 3131
QY 945 leThrGlnAlaGluIleGluSerIleValLysProLysValLeuGluLysGluAlaGluL 965
Db 3132 --ACTCAAGCAGAGATAGAGCATAGTATTAAACCAAGTTCTTGTGAAGAGCTGAGA 3189
QY 965 ysLysLeuProSerAspThrGluLysGluAspArgSerProSerAlaIlePheSerAlaA 985
Db 3190 AAAAATTTCTTCCGATACAGAAAAGAGGACAGATCACCATCTGCTATATTTTCAGCAG 3249
QY 985 pLeu-GlyLysThrSerValValAspLeuLeuTyrTrpArgAspIleLysLysThrGly 1004
Db 3250 AGCTGAGCTAAATCTAGTTGCTTACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3309
QY 1005 ValValPheGlyAlaSerLeuPheLeuLeuLeuSerLeuThrValPheSerIleValSer 1024
Db 3310 GTGGGTGTTGGTGCCAGCTATCTCTGCTGCTTTCATTGACAGTATTCAGCATTTGTGAGC 3369
QY 1025 ValThrAlaTyrIleAlaLeuAlaLeuSerValThrIleSerPheArgIleTyrLys 1044
Db 3370 GTAACAGCCTACATTCGCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAG 3429
QY 1045 GlyValIleGlnAlaIleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGlu 1064
Db 3430 GGTGTGATCCAAAGCTATCCAGAAATCAGATGAAGGCCACCCATTCAGGCGCATATCTGAA 3489
QY 1065 SerGluValAlaIleSerGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHis 1084
Db 3490 TCTGAAGTTGTGATATCTGAGAGTGGGTTCAGAAAGTACAGTAATCTGCTCTTGGTCAT 3549
QY 1085 ValAsnCysThrIleLysGluLeuArgArgLeuPheLeuValAspLeuValAspSer 1104
Db 3550 GTGAAGTGCACGATAAAGAACTCAGGCGCTCTTCTTAGTTGATGATTTAGTTGATTTCT 3609
QY 1105 LeuLysPheAlaValLeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeu 1124
Db 3610 CTGAAGTTTGCAGTGTGTGATGGGTATTTACCTATGTTGGTGCCTTGTGTTAATGGTCTG 3669
QY 1125 ThrLeuLeuIleLeuAlaLeuIleSerLeuPheSerValProValIleTyrGluArgHis 1144
Db 3670 ACACACTAGTATTTGGCTCTCATTTTCATCTTCCTCAGTGTTCCTGTTATTATTAAGCGGCAT 3729
QY 1145 GlnAlaGlnIleAspHisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAla 1164
Db 3730 CAGGCACAGATAGATCATTTATCTAGGACTTGCAATAGAAATGTAAGATGCTATGGCT 3789
QY 1165 LysIleGlnAlaLysIleProGlyLeuLysArgLysAlaGlu 1178
Db 3790 AAAATCCAAAGCAAAATCCCTGGATTGAAGCGCAAGCTGAA 3831

RESULT 2
abs70449/c
; TOIG of: abs70449 check: 9399 from: 1 to: 4822
; ID ABS70449 standard; cDNA; 4822 BP.
; XX
; AC ABS70449;
; XX

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; DT 27-NOV-2002 (first entry)
; XX Human bone remodelling gene #106.
; XX
; KW Bone remodelling; osteoporosis; human; gene; ss.
; XX
; OS Homo sapiens.
; XX
; PN US6426186-B1.
; XX
; PD 30-JUL-2002.
; XX
; PF 18-JAN-2000; 2000US-00484970.
; XX
; PR 18-JAN-2000; 2000US-00484970.
; XX
; PA (INCYTE GENOMICS INC.
; XX
; PI Jones KA, Volkmutch W, Walker MG;
; XX
; DR WPI; 2002-673014/72.
; XX
; AB A combination of polynucleotides which are co-expressed with genes known
; PT to be involved in bone remodeling and osteoporosis are useful in an array
; PT for the diagnosis of bone remodeling and osteoporosis associated
; XX disorders.
; XX
; PS Claim 1; Col 283-288; 206pp; English.
; XX
; CC The invention relates to a combination comprising a number of
; CC substantially purified and isolated polynucleotides which are co-
; CC expressed with genes known to be involved in bone remodeling and
; CC osteoporosis. The invention is used to diagnose disorders associated with
; CC bone remodeling or osteoporosis. ABS70344-ABS70512 represent human bone
; CC remodelling genes of the invention
; XX
; SQ Sequence 4822 BP; 1441 A; 1046 C; 1073 G; 1247 T; 0 U; 15 Other;
;
; ABS70449 Length: 4822 June 22, 2005 09:05 Type: N Check: 9399 ..
abs70449

Alignment Scores:
Pred. No.: 0 Length: 4822
Score: 96.00 Matches: 42
Percent Similarity: 31.93% Conservative: 11
Best Local Similarity: 25.30% Mismatches: 61
Query Match: 1.62% Indels: 52
DB: 1 Gaps: 7

US-09-830-972-29-COPY (1-1178) x abs70449 (1-4822)
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Db 703 CGCTGCCCGGGAGGAGGGGAGGCGCGCGGAGGCTCGTCTCCTCAGGAGCTTGG 644
QY 49 LeuGluGluLeuGluValLeuGluArgLysProAlaGlyLeuSerAlaAlaProVal 68
Db 643 AGGCGCAGACTG-----CGGCAGCAGACAGCGGGGATGCGCGGCACGG--- 599
QY 69 ProThrAlaProAlaAlaGlyAlaProLeuMetAspPheGlyAsnAspPheValPro 88
Db 598 TGCAGCAGACCGGGCTCGGGTCCC-----AAGACGGCTCGCGCTCCG 557
QY 89 AlaProArgGlyProLeuProAlaAlaProProValAlaPro----- 102
Db 556 GGGCGACGGGGGAGCGCGCGGAGGCTCCCGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 497
QY 103 -----GluArgGlnProSerTrpAspProSerProValSerSer 115
Db 496 CGAAGTCCATTANNNGCGCGCGGAGGCGGCTGGGCACACTGGGGCGCGCGCGCGCGCGCGCG 437
QY 116 ThrValProAlaProSerProLeuSerAlaAlaAlaValSerProSerLysLeuProGlu 135

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Db      436 CGCGCGCGGCTTCCTCT----- 419
Qy      136 AspAspGluProProAlaArgProProProProProAlaSerValSerProGlnAla 155
Db      418 -----CCAGCACCTCCAGCTCCTCCAGGTCTTCGTCTCTCGT--- 383
Qy      156 GluProValTrpThrProProAlaProAlaProAlaProAlaProSerThrProAlaAla 175
Db      382 -----CCTCCTCTTCATCCTCTCTCTCTCTCTCT---CGTCCTCGGGCT 341
Qy      176 ProlysArgArgGlySer 181
Db      340 CCCTCAGCAACTGGTACT 323

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Search completed: June 22, 2005, 09:12:28
Job time : 23 secs